REMARKS

Applicant has amended claims 1-8 to remove informalities, which moots the examiner's indefiniteness rejections. Applicant has canceled claims 9-20 as being directed to non-elected subject matter, and has added claims 21-41. Upon entry of this amendment, claims 1-8 and 21-41 will be pending. A marked-up copy of the amended claims is attached.

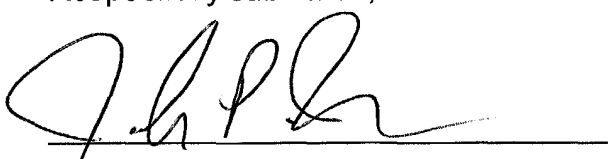
Support for the amended and added claims can be found throughout the specification. Paragraphs 0002, 0009-0012 and 0020 of the specification discuss the differences between encapsulated and free nucleic acids, the usefulness of nucleases in distinguishing these types of nucleic acids, how inactivated pathogens yield free nucleic acids, and how free nucleic acids cannot be detected following nuclease treatment. However, encapsulated nucleic acids cannot be attacked by the nuclease, and thus nucleic acid content detected in the digested sample is representative of infectious pathogens being present in the tested sample. See paragraph 0012

Thus, the instant invention has all of the advantages of nucleic acid amplification methods, such as sensitivity and the ability to detect difficult to cultivate pathogens, while avoiding the pitfalls of amplification, namely false positives caused by non-infectious forms of the pathogen in the sample (*e.g.,* free DNA from disrupted virions). For example, biological products that contain free pathogen DNA (which is non-infectious) would nevertheless be destroyed under prior art practices. See paragraphs 0003, 0006 and 0015 of the specification. Accordingly, the present invention permits to production of safe samples in a more efficient manner than previous practices.

Request

Applicants submit that the claims are in condition for allowance, and respectfully request favorable consideration to that effect. The examiner is invited to contact the undersigned at (202) 912-2000 should there be any questions.

Respectfully submitted,



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Marked-up Copy of Amended Claims

1. (Amended) A method for **[detection, differentiation and quantification of]** **determining the type of target nucleic acids in a sample, wherein the method is capable of differentiating** free and encapsulated target nucleic acids in **[a]** **the** sample, **wherein the method comprises** **[comprising]**

(a) determining a total target nucleic acid content in **[said]** **the** sample**[,]** **;**

(b) adding a nuclease to **[said]** **the** sample to digest free target nucleic acids in **[said]** **the** sample to form a digested sample;

(c) determining a total target nucleic acid **content** remaining in **[said]** **the** digested sample; and

(d) quantifying the total amount of free target nucleic acid in **[said]** **the** sample by **[subtraction of said]** **subtracting the** determined **amount of** target nucleic acid content in **[said]** **the** digested sample from **[said]** **the** determined **amount of total** target nucleic acid content in **[said]** **the** sample.

2. (Amended) The method of claim 1**,** wherein **[said]** **the** determining of **[said]** **the** target nucleic acids is performed using a nucleic acid amplification assay.

3. (Amended) The method of claim 2**,** wherein **[said]** **the** nucleic acid amplification **[assays]** **assay** is a polymerase chain reaction (PCR) assay or a reverse transcriptase (RT) PCR assay.

4. (Amended) The method of claim 1, further comprising adding **a** nucleic acid standard to **[said] the** sample before **[said] the [first]** total target nucleic acid content **of (a)** is determined.

5. (Amended) The method of claim 1, further comprising adding **a** nucleic acid standard to **[said] the** sample after **the** free target nucleic acid**s** in **[said] the** sample are digested with **[said] the** nuclease.

6. (Amended) The method of claim 1, wherein **[said] the** nuclease is inactivated after **[said] the** free nucleic acids in **[said] the** sample are digested.

7. (Amended) The method of claim 1, wherein **[said] the** nuclease is **a** DNase or **an** RNase.

8. (Amended) The method of claim 1, wherein **[said] the** sample is selected from the group consisting of blood, plasma, serum, cell culture fluids, cells and a pharmaceutical preparation.